

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Vandlen, Richard J.
Holmes, William E.

(ii) TITLE OF INVENTION: Structure, Production and Use of
Heregulin 2 Ligands

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 24-MAY-1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Benson, Robert H.
(B) REGISTRATION NUMBER: 30,446
(C) REFERENCE/DOCKET NUMBER: 712

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/266-1489
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 CXCAAT 6

10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

20 AATAAA 6

25 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa
1 5 10 15

35 Phe Met Val Lys Asp Leu Xaa Asn Pro
20 24

40 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys
1 5 10 15

50 Glu Xaa Gly Xaa Gly Lys
20 21

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Glu Lys Glu Lys Thr Phe Xaa Val Asn Gly Gly Glu
1 5 10 13

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTGAGAAGG AGAAGACCTT CTGTCGTGAA TCGGACGGCG AG 42

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Xaa Arg Gln Pro Lys Tyr Pro Arg Lys Ser Ala Pro Arg Arg
1 5 10 15

Asn Lys Leu Asp His Tyr Ala Ile Ile Lys Phe Pro Leu Thr
20 25 29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGCAGCCCA AGTACCCCXG GAAGTCCGCC CCCXGGXGGA ACAAGCT 47

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCTTGTTCTGA XCTGGTGATA CGGTAGTAGT TGAAGGGGGA C 41

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2010 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GG GCG CGA GCG CCT CAG CGC GGC CGC TCG CTC TCC CCC 38
Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro
1 5 10

TCG AGG GAC AAA CTT TTC CCA AAC CCG ATC CGA GCC CTT 77
Ser Arg Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu
15 20 25

GGA CCA AAC TCG CCT GCG CCG AGA GCC GTC CGC GTA GAG 116
Gly Pro Asn Ser Pro Ala Pro Arg Ala Val Arg Val Glu
30 35

CGC TCC GTC TCC GGC GAG ATG TCC GAG CGC AAA GAA GGC 155
Arg Ser Val Ser Gly Glu Met Ser Glu Arg Lys Glu Gly
40 45 50

AGA GGC AAA GGG AAG GGC AAG AAG AAG GAG CGA GGC TCC 194
Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser
55 60

GGC AAG AAG CCG GAG TCC GCG GCG GGC AGC CAG AGC CCA 233
Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro
65 70 75

GCC TTG CCT CCC CGA TTG AAA GAG ATG AAA AGC CAG GAA 272
Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
80 85 90

TCG GCT GCA GGT TCC AAA CTA GTC CTT CGG TGT GAA ACC 311
 Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr
 95 100

5 AGT TCT GAA TAC TCC TCT CTC AGA TTC AAG TGG TTC AAG 350
 Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys
 105 110 115

10 AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA CCA CAA AAT 389
 Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn
 120 125

15 ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC 428
 Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg
 130 135 140

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG 467
 Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 145 150 155

20 TGC AAA GTG ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT 506
 Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
 160 165

25 GCC AAT ATC ACC ATC GTG GAA TCA AAC GAG ATC ATC ACT 545
 Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile Thr
 170 175 180

30 GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT TCA 584
 Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser
 185 190

35 GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA 623
 Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 195 200 205

AAT ACT TCT TCA TCT ACA TCT ACA TCC ACC ACT GGG ACA 662
 Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 210 215 220

40 AGC CAT CTT GTA AAA TGT GCG GAG AAG GAG AAA ACT TTC 701
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe
 225 230

45 TGT GTG AAT GGA GGG GAG TGC TTC ATG GTG AAA GAC CTT 740
 Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu
 235 240 245

50 TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC CAA CCT GGA 779
 Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly
 250 255

55 TTC ACT GGA GCA AGA TGT ACT GAG AAT GTG CCC ATG AAA 818
 Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 260 265 270

GTC CAA AAC CAA GAA AAG GCG GAG GAG CTG TAC CAG AAG 857
 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys

275 280 285
 AGA GTG CTG ACC ATA ACC GGC ATC TGC ATC GCC CTC CTT 896
 Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu
 290 295
 5
 GTG GTC GGC ATC ATG TGT GTG GTG GCC TAC TGC AAA ACC 935
 Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr
 300 305 310
 10
 AAG AAA CAG CGG AAA AAG CTG CAT GAC CGT CTT CGG CAG 974
 Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln
 315 320
 15
 AGC CTT CGG TCT GAA CGA AAC AAT ATG ATG AAC ATT GCC 1013
 Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala
 325 330 335
 20
 AAT GGG CCT CAC CAT CCT AAC CCA CCC CCC GAG AAT GTC 1052
 Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val
 340 345 350
 CAG CTG GTG AAT CAA TAC GTA TCT AAA AAC GTC ATC TCC 1091
 Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
 355 360
 25
 AGT GAG CAT ATT GTT GAG AGA GAA GCA GAG ACA TCC TTT 1130
 Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe
 365 370 375
 30
 TCC ACC AGT CAC TAT ACT TCC ACA GCC CAT CAC TCC ACT 1169
 Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
 380 385
 35
 ACT GTC ACC CAG ACT CCT AGC CAC AGC TGG AGC AAC GGA 1208
 Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly
 390 395 400
 40
 CAC ACT GAA AGC ATC CTT TCC GAA AGC CAC TCT GTA ATC 1247
 His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
 405 410 415
 45
 GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC CCA 1286
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
 420 425
 ACT GGG GGC CCA AGA GGA CGT CTT AAT GGC ACA GGA GGC 1325
 Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly
 430 435 440
 50
 CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA 1364
 Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu
 445 450
 55
 ACC CCT GAT TCC TAC CGA GAC TCT CCT CAT AGT GAA AGG 1403
 Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
 455 460 465

5 TAT GTG TCA GCC ATG ACC ACC CCG GCT CGT ATG TCA CCT 1442
 Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
 470 475 480

10 GTA GAT TTC CAC ACG CCA AGC TCC CCC AAA TCG CCC CCT 1481
 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro
 485 490

15 TCG GAA ATG TCT CCA CCC GTG TCC AGC ATG ACG GTG TCC 1520
 Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser
 495 500 505

20 ATG CCT TCC ATG GCG GTC AGC CCC TTC ATG GAA GAA GAG 1559
 Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu
 510 515

25 AGA CCT CTA CTT CTC GTG ACA CCA CCA AGG CTG CGG GAG 1598
 Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
 520 525 530

30 AAG AAG TTT GAC CAT CAC CCT CAG CAG TTC AGC TCC TTC 1637
 Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe
 535 540 545

35 CAC CAC AAC CCC GCG CAT GAC AGT AAC AGC CTC CCT GCT 1676
 His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala
 550 555

40 AGC CCC TTG AGG ATA GTG GAG GAT GAG GAG TAT GAA ACG 1715
 Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr
 560 565 570

45 ACC CAA GAG TAC GAG CCA GCC CAA GAG CCT GTT AAG AAA 1754
 Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys
 575 580

50 CTC GCC AAT AGC CGG CGG GCC AAA AGA ACC AAG CCC AAT 1793
 Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn
 585 590 595

55 GGC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC ACA 1832
 Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr
 600 605 610

60 AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT 1871
 Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp
 615 620

65 GAA AGA GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG 1910
 Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln
 625 630 635

70 AAC CCC CTG GCA GCC AGT CTT GAG GCA ACA CCT GCC TTC 1949
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe
 640 645

75 CGC CTG GCT GAC AGC AGG ACT AAC CCA GCA GGC CGC TTC 1988
 Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe

650

655

660

TCG ACA CAG GAA GAA ATC CAG G 2010
 Ser Thr Gln Glu Glu Ile Gln
 665 669

5

(2) INFORMATION FOR SEQ ID NO:11:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 669 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro Ser Arg Asp
 1 5 10 15
 Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro
 20 25 30
 Ala Pro Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met
 35 40 45
 Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 50 55 60
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln
 65 70 75
 Ser Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
 80 85 90
 Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 95 100 105
 Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu
 110 115 120
 Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys
 125 130 135
 Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp
 140 145 150
 Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
 155 160 165
 Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Glu Ile Ile
 170 175 180
 Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser Ser Glu
 185 190 195

	Ser Pro Ile Arg	Ile Ser Val Ser Thr	Glu Gly Ala Asn Thr Ser	200	205	210
5	Ser Ser Thr Ser	Thr Ser Thr Thr Gly	Thr Ser His Leu Val Lys	215	220	225
	Cys Ala Glu Lys	Glu Lys Thr Phe Cys	Val Asn Gly Gly Glu Cys	230	235	240
10	Phe Met Val Lys	Asp Leu Ser Asn Pro	Ser Arg Tyr Leu Cys Lys	245	250	255
	Cys Gln Pro Gly	Phe Thr Gly Ala Arg	Cys Thr Glu Asn Val Pro	260	265	270
15	Met Lys Val Gln	Asn Gln Glu Lys Ala	Glu Glu Leu Tyr Gln Lys	275	280	285
	Arg Val Leu Thr	Ile Thr Gly Ile Cys	Ile Ala Leu Leu Val Val	290	295	300
20	Gly Ile Met Cys	Val Val Ala Tyr Cys	Lys Thr Lys Lys Gln Arg	305	310	315
25	Lys Lys Leu His	Asp Arg Leu Arg Gln	Ser Leu Arg Ser Glu Arg	320	325	330
	Asn Asn Met Met	Asn Ile Ala Asn Gly	Pro His His Pro Asn Pro	335	340	345
30	Pro Pro Glu Asn	Val Gln Leu Val Asn	Gln Tyr Val Ser Lys Asn	350	355	360
35	Val Ile Ser Ser	Glu His Ile Val Glu	Arg Glu Ala Glu Thr Ser	365	370	375
	Phe Ser Thr Ser	His Tyr Thr Ser Thr	Ala His His Ser Thr Thr	380	385	390
40	Val Thr Gln Thr	Pro Ser His Ser Trp	Ser Asn Gly His Thr Glu	395	400	405
	Ser Ile Leu Ser	Glu Ser His Ser Val	Ile Val Met Ser Ser Val	410	415	420
45	Glu Asn Ser Arg	His Ser Ser Pro Thr	Gly Gly Pro Arg Gly Arg	425	430	435
	Leu Asn Gly Thr	Gly Gly Pro Arg Glu	Cys Asn Ser Phe Leu Arg	440	445	450
50	His Ala Arg Glu	Thr Pro Asp Ser Tyr	Arg Asp Ser Pro His Ser	455	460	465

	Glu	Arg	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	
					470					475					480	
5	Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	
					485					490					495	
	Met	Ser	Pro	Pro	Val	Ser	Ser	Met	Thr	Val	Ser	Met	Pro	Ser	Met	
					500					505					510	
10	Ala	Val	Ser	Pro	Phe	Met	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	
					515					520					525	
	Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Lys	Phe	Asp	His	His	Pro	Gln	
15					530					535					540	
	Gln	Phe	Ser	Ser	Phe	His	His	Asn	Pro	Ala	His	Asp	Ser	Asn	Ser	
					545					550					555	
20	Leu	Pro	Ala	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	Glu	Tyr	Glu	
					560					565					570	
	Thr	Thr	Gln	Glu	Tyr	Glu	Pro	Ala	Gln	Glu	Pro	Val	Lys	Lys	Leu	
					575					580					585	
25	Ala	Asn	Ser	Arg	Arg	Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile	
					590					595					600	
	Ala	Asn	Arg	Leu	Glu	Val	Asp	Ser	Asn	Thr	Ser	Ser	Gln	Ser	Ser	
					605					610					615	
	Asn	Ser	Glu	Ser	Glu	Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	
					620					625					630	
35	Pro	Phe	Leu	Gly	Ile	Gln	Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	
					635					640					645	
	Thr	Pro	Ala	Phe	Arg	Leu	Ala	Asp	Ser	Arg	Thr	Asn	Pro	Ala	Gly	
					650					655					660	
40	Arg	Phe	Ser	Thr	Gln	Glu	Glu	Ile	Gln							
					665				669							

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val
1				5				10						15

Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser
 20 25 30
 5 Arg Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys
 35 40 45
 Thr Glu Asn Val Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu
 50 55 60
 10 Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile
 65 70 75
 15 Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys
 80 85 90
 Thr Lys Lys Gln Arg
 95

20 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu
 1 5 10 15
 His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala
 20 25 30
 35 Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg
 35 40 45
 Asp Leu Lys Trp Trp Glu Leu Arg His Ala Gly His Gly Gln Gln
 50 55 60
 40 Gln Lys Val Ile Val Val Ala Val Cys Val Val Val Leu Val Met
 65 70 75
 45 Leu Leu Leu Leu Ser Leu Trp Gly Ala His Tyr Tyr Arg Thr Gln
 80 85 90
 Lys
 91

50 (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 Asn Asp Cys Pro Asp Ser His Thr Gln Phe Cys Phe His Gly Thr
1 5 10 15
Cys Arg Phe Leu Val Gln Glu Asp Lys Pro Ala Cys Val Cys His
20 25 30
10 Ser Gly Tyr Val Gly Ala Arg Cys Glu His Ala Asp Leu Leu Ala
35 40 45
Val Val Ala Ala Ser Gln Lys Lys Gln Ala Ile Thr Ala Leu Val
15 50 55 60
Val Val Ser Ile Val Ala Leu Ala Val Leu Ile Ile Thr Cys Val
65 70 75
20 Leu Ile His Cys Cys Gln Val
80 82

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25 Lys Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile
1 5 10 15
35 His Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys
20 25 30
Lys Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser
35 40 45
40 Met Lys Thr His Ser Met Ile Asp Ser Ser Leu Ser Lys Ile Ala
50 55 60
Leu Ala Ala Ile Ala Ala Phe Met Ser Ala Val Ile Leu Thr Ala
45 65 70 75
Val Ala Val Ile Thr Val Gln Leu Arg Arg Gln Tyr
80 85 87

50 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 Lys Lys Lys Asn Pro Cys Ala Ala Lys Phe Gln Asn Phe Cys Ile
1 5 10 15
His Gly Glu Cys Arg Tyr Ile Glu Asn Leu Glu Val Val Thr Cys
20 25 30
10 His Cys His Gln Asp Tyr Phe Gly Glu Arg Cys Gly Glu Lys Thr
35 40 45
15 Met Lys Thr Gln Lys Lys Asp Asp Ser Asp Leu Ser Lys Ile Ala
50 55 60
Leu Ala Ala Ile Ile Val Phe Val Ser Ala Val Ser Val Ala Ala
65 70 75
20 Ile Gly Ile Ile Thr Ala Val Leu Leu Arg Lys Arg
80 85 87

(2) INFORMATION FOR SEQ ID NO:17:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile
1 5 10 15
35 His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30
Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser
35 40 45
40 Leu Pro Val Glu Asn Arg Leu Tyr Thr Tyr Asp His Thr Thr Ile
50 55 60
45 Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu Val
65 70 75
Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg
80 85 86

50